

Fig. 1

Human glycoprotein hormone β 10 polypeptide:

MKLAFLFLGPMALLLAGYGCVLGASSG¹NLR²TFVGCAVREF³FLAKPKGRGLR⁴ITTDACWGRCE⁵TWEKPILEPPYIEAHRVCTY⁶N⁷ETKQVTVKLENCAPGVDPFYTPVAIRCDGACSTATTECETI⁸

Nucleic acid encoding human glycoprotein hormone β 10 polypeptide:

ATGAAGCTGGCATTCCTCTTCCCTTGGCCCCCATGGCCCTCCTCTCTGGC
TGGCTATGGCTGTGTCCTCGGTGCCCTCCAGTGGGAACCTGCGCACCTTTG
TGGCTGTGCCGTGAGGGAGTTTACTTTCCTGGCCAAAGAACCCAGGCTGC
AGGGCCCTTCGGATCACACGGATGCCCTGCTGGGTGCTGTGAGACCTG
GGAGAAACCCATTCTGGAACCCCTATATGAAGCCCATCATCGAGTCT
GTACCTACAACGAGACCAACAGGTGACTGTCAAGTGGCCCAACTGTGCC
CCGGAGTCGACCCCTTCTACACCTATCCGTGGCCATCCGCTGTGACTG
CGGAGCCCTGCTCCACTGCCACCCACGGAGTGTGAGACCATCTGAGGCCGCT
AGCTGCTCTCTGCAGACCCACCTGTGTGAGCAGCACATGC

Fig. 2A

GAP OF: HUMAN TSH- β CHECK: 4247 FROM: 1 TO: 118
 TO: HUMAN β 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:
 /GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP
 COMPCHECK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	140	LENGTH:	129
RATIO:	1.321	GAPS:	4
PERCENT SIMILARITY:	47.368	PERCENT IDENTITY:	36.842

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):
 | = IDENTITY
 : = 2
 . = 1

HUMAN TSH- β X HUMAN β 10

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1 .....FCIPTEYTMHIERRECA YCLTINTTICAGYCMTRDINGK L 40
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCETWE..KPI 47

41 FLPKYALSQD.VCTYRDFIYRTVEIPGCPLHVAPYFSYPVALSCKCGKCN 89
      | | . | | | | : | | : | | | | | | | | | | | | | | | |
48 LEPPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDCGACS 97

90 TDYSDCIHEAIKTN YCTKPQKSYLVGFSV 118
      | . : | | |
98 TATTEC..ETI..... 106
  
```

Fig. 2B

GAP OF: HUMAN FSH- β CHECK: 8841 FROM: 1 TO: 111
 TO: HUMAN β 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:
 /GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP
 COMPCHECK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	156	LENGTH:	122
RATIO:	1.472	GAPS:	3
PERCENT SIMILARITY:	44.211	PERCENT IDENTITY:	35.789

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):
 | = IDENTITY
 : = 2
 . = 1

HUMAN FSH- β X HUMAN β 10

```

1 .....NSCELTNITIAIEKEEERFCISINTTWCAGYCYTRDL.VYK 40
      | . | . | | : | | | | | : : .
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCEWKEKPILE 49

41 DPARPKIQKTCTFKELVYETVRVPGCAHHADSLYTPVATQCHCGKCDSD 90
      | : ||: | ||: . | | | | | | . | | | .
50 PPYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTPVAIRCDCGACSTA 99

91 STDC.TVRGLGPSYCSFGEMKE 111
      .|:| |:
100 TTECETI..... 106
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[illegible]

TO: HUMAN β 10 CHECK: 6611 FROM: 1 TO: 106

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	140	LENGTH:	125
RATIO:	1.321	GAPS:	3
PERCENT SIMILARITY:	44.118	PERCENT IDENTITY:	32.353

HUMAN LH- β X HUMAN β 10

```

1  .SREPLRPW..CHPINAILAVEKEGCPVCITVNTTICAGYCPPTMMR.VLQ 46
   | | | | . | | | | | : : | | | | : : | :
1  ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCEWKEPIL 49
   | | | | | | | | | | | | | | | | | | | | | |
47  AVLPLPLPQVVCTYRDVRFESIRLPGCPRGVDPVVSFPVALSCRCGPCRRS 96
   | | | | : : . : | | | | | | | | . : | | | : | | | | .
50  PPYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDGACSTA 99
   | | | | | | | | | | | | | | | | | | | | | |
97  TSDCGGPKDHPLTCDHPQLSGLLFL 121
   | . : |
100 TTECETI..... 106

```

Fig. 2D

GAP OF: HUMAN CG- β CHECK: 2358 FROM: 1 TO: 145

TO: HUMAN β 10 CHECK: 6611 FROM: 1 TO: 106

SYMBOL COMPARISON TABLE:
/GCGDISK/GCG10/GCGCORE/DATA/RUNDATA/BLOSUM62.CMP
COMPCHK: 6430

GAP WEIGHT:	8	AVERAGE MATCH:	2.912
LENGTH WEIGHT:	2	AVERAGE MISMATCH:	-2.003
QUALITY:	131	LENGTH:	149
RATIO:	1.236	GAPS:	3
PERCENT SIMILARITY:	42.157	PERCENT IDENTITY:	31.373

MATCH DISPLAY THRESHOLDS FOR THE ALIGNMENT(S):
| = IDENTITY
: = 2
. = 1

HUMAN CG- β X HUMAN β 10

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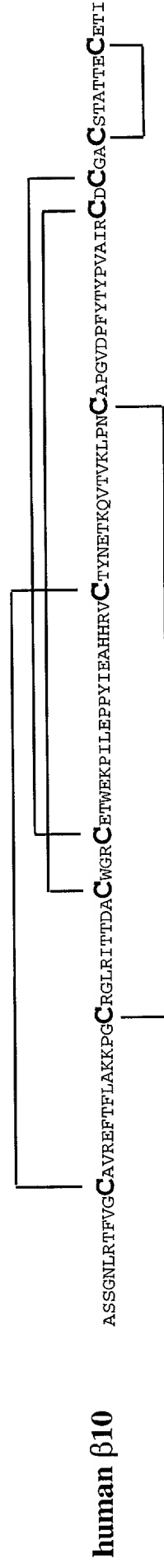
1 .SKEPLRP..RCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTR.VLQ 46
  ||  ||  |  |  .|  ||  :  :  |  |  |  |  |  :  :  |
1 ASSGNLRTFVGCAVREFTFLAKKPGCR.GLRITTDACWGRCEWKEKPILE 49

47 GVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRS 96
  ||  |  :  :  .::||  |  ||.  |  .|  ||:  |  |  |  .
50 PPYIEAHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDGACSTA 99

97 TTDCGGPKDHPLTCDDPRFQDSSSSKAPPPSLPSRLPGPSDTPILPQ 145
  ||:|
100 TTECETI..... 106
  
```

FOAFO "HSEFSE"

Fig. 3



— = Disulfide bond

[illegible]

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1 ASSGNLRTFVGCAREFTFLAKKPGCRLRITTDACWGRCEWEKPILEP 50
. ||||| : |||||
1 SSSGNLHTFVGCAREFTFMAKKPGCRLRITTDACWGRCEWEKPILEP 50

51 PYIEAHHRVCTYNETKQVTVKLPNCAPGVDPFYTYPVAIRCDCGACSTAT 100
||||| : ||||| . : |||||
51 PYIEAYHRVCTYNETRQVTVKLPNCAPGVDPFYTPMAVRDCGACSTAT 100

101 TECETI 106
|||||
101 TECETI 106
```